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SEP 30 2003

TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

DATE: 09/25/2003

PATENT APPLICATION: US/09/874,389B

TIME: 14:14:58

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\09252003\I874389B.raw

4 <110> APPLICANT: BUJARD, Hermann
 5 GOSSEN, Manfred
 7 <120> TITLE OF INVENTION: Transgenic Organisms Having Tetracycline-Regulated
 Transcriptional

8 Regulatory Systems (as amended)
 11 <130> FILE REFERENCE: BBI-009C3CN2
 13 <140> CURRENT APPLICATION NUMBER: 09/874389B
 14 <141> CURRENT FILING DATE: 2001-06-04
 16 <150> PRIOR APPLICATION NUMBER: 09/161902
 17 <151> PRIOR FILING DATE: 1998-09-28
 19 <150> PRIOR APPLICATION NUMBER: 08/487472
 20 <151> PRIOR FILING DATE: 1995-06-07
 22 <150> PRIOR APPLICATION NUMBER: 08/383754
 23 <151> PRIOR FILING DATE: 1995-02-03
 25 <150> PRIOR APPLICATION NUMBER: 08/275876
 26 <151> PRIOR FILING DATE: 1994-07-15
 28 <150> PRIOR APPLICATION NUMBER: 08/270637
 29 <151> PRIOR FILING DATE: 1994-07-01
 31 <150> PRIOR APPLICATION NUMBER: 08/260452
 32 <151> PRIOR FILING DATE: 1994-06-14
 34 <150> PRIOR APPLICATION NUMBER: 08/076327
 35 <151> PRIOR FILING DATE: 1993-06-14
 37 <150> PRIOR APPLICATION NUMBER: 08/076726
 38 <151> PRIOR FILING DATE: 1993-06-14
 40 <160> NUMBER OF SEQ ID NOS: 28
 42 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 44 <210> SEQ ID NO: 1
 45 <211> LENGTH: 1008
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Artificial Sequence
 49 <220> FEATURE:
 50 <223> OTHER INFORMATION: Tet activator fusion
 52 <220> FEATURE:
 53 <221> NAME/KEY: exon
 54 <222> LOCATION: (1)...(1008)
 56 <220> FEATURE:
 57 <221> NAME/KEY: mRNA
 58 <222> LOCATION: (1)...(1008)
 60 <220> FEATURE:
 61 <221> NAME/KEY: misc_binding
 62 <222> LOCATION: (1)...(207)
 64 <220> FEATURE:
 65 <221> NAME/KEY: misc_binding
 66 <222> LOCATION: (208)...(335)

ENTERED

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68 <220> FEATURE:

69 <221> NAME/KEY: CDS

70 <222> LOCATION: (1)...(1005)

74 <400> SEQUENCE: 1

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75 atg tct aga tta gat aaa act aaa gtg att aac agc gca tta gag ctg      48
76 Met Ser Arg Leu Asp Lys Thr Lys Val Ile Asn Ser Ala Leu Glu Leu
77 1          5          10          15
79 ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag      96
80 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
81          20          25          30
83 aag cta ggt gta gag cag cct aca ctg tat tgg cat gta aaa aat aag      144
84 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
85          35          40          45
87 cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat      192
88 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
89          50          55          60
91 act cac ttt tgc cct tta aaa ggg gaa agc tgg caa gat ttt tta cgc      240
92 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
93 65          70          75          80
95 aat aag gct aaa agt ttt aga tgt gct tta cta act cat cgc aat gga      288
96 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Thr His Arg Asn Gly
97          85          90          95
99 gca aaa gta cat tca gat aca cgg cct aca gaa aaa cag tat gaa act      336
100 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
101          100          105          110
103 ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag      384
104 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
105          115          120          125
107 aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc      432
108 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
109          130          135          140
111 gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca      480
112 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
113 145          150          155          160
115 cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta      528
116 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
117          165          170          175
119 ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg      576
120 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
121          180          185          190
123 atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tcc gcg      624
124 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
125          195          200          205
127 tac agc cgc gcg cgt acg aaa aac aat tac ggg tct acc atc gag ggc      672
128 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
129          210          215          220
131 ctg ctc gat ctc ccg gac gac gac gcc ccc gaa gag gcg ggg ctg gcg      720
132 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
133 225          230          235          240

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```

135 gct ccg cgc ctg tcc ttt ctc ccc gcg gga cac acg cgc aga ctg tcg 768
136 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
137          245          250          255
139 acg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac 816
140 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
141          260          265          270
143 ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat 864
144 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
145          275          280          285
147 ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 912
148 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
149          290          295          300
151 cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 960
152 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
153 305          310          315          320
155 gag cag atg ttt acc gat ccc ctt gga att gac gag tac ggt ggg 1005
156 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
157          325          330          335
159 tag 1008
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 335
163 <212> TYPE: PRT
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: mutated Tn-10 derived Tet repressor
169 <400> SEQUENCE: 2
170 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
171 1 5 10 15
172 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
173 20 25 30
174 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
175 35 40 45
176 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
177 50 55 60
178 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
179 65 70 75 80
180 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
181 85 90 95
182 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
183 100 105 110
184 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
185 115 120 125
186 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
187 130 135 140
188 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
189 145 150 155 160
190 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
191 165 170 175
192 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu

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```

193          180          185          190
194 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
195          195          200          205
196 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
197          210          215          220
198 Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
199 225          230          235          240
200 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
201          245          250          255
202 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
203          260          265          270
204 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
205          275          280          285
206 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
207          290          295          300
208 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
209 305          310          315          320
210 Glu Gly Met Phe Thr Asp Pro Leu Gly His Asp Glu Tyr Gly Gly
211          325          330          335
214 <210> SEQ ID NO: 3
215 <211> LENGTH: 33
216 <212> TYPE: DNA
217 <213> ORGANISM: Herpes simplex virus
219 <220> FEATURE:
220 <221> NAME/KEY: CDS
221 <222> LOCATION: (1)...(33)
223 <400> SEQUENCE: 3
224 gac gcg cta gac gat ttc gat ctg gac atg ttg 33
227 <210> SEQ ID NO: 4
228 <211> LENGTH: 11
229 <212> TYPE: PRT
230 <213> ORGANISM: Herpes simplex virus
232 <400> SEQUENCE: 4
233 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
234 1 5 10
237 <210> SEQ ID NO: 5
238 <211> LENGTH: 7
239 <212> TYPE: PRT
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: nuclear localization signal
245 <400> SEQUENCE: 5
246 Met Pro Lys Arg Pro Arg Pro
247 1 5
250 <210> SEQ ID NO: 6
251 <211> LENGTH: 569
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:

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Input Set : A:\PTO.YF.txt

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256 <223> OTHER INFORMATION: Bidirectional promoter

258 <400> SEQUENCE: 6

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259 gaattcgggg ccgcggaggc tggatcggtc ccggtgtctt ctatggaggt caaaacagcg 60
260 tggatggcgt ctccaggcga tctgacggtt cactaaacga gctctgctta tataggctga 120
261 gtttaccact ccctatcagt gatagagaaa agtgaaagtc gagtttacca ctccctatca 180
262 gtgatagaga aaagtgaaag tcgagtttac cactccctat cagtgataga gaaaagtga 240
263 agtcgagttt accactccct accagtgata gagaaaagtg aaagtcgagt ttaccactcc 300
264 ctatcagtga tagagaaaaa tgaaagtcga gtttaccact ccctatcagt gatagagaaa 360
265 agtgaaagtc gagtttacca ctccctatca gtgatagaga aaagtgaaag tcgagctcgg 420
266 taccggggtc gagtaggcgt gtacggtggg aggcctatat aagcagagct cgtttagtga 480
267 accgtcagat cgcttgaga cgccatccac gctgttttga cctccataga agacaccggg 540
268 accgatccag cctccgcggc cccgaattc 569

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270 <210> SEQ ID NO: 7

271 <211> LENGTH: 520

272 <212> TYPE: DNA

273 <213> ORGANISM: Artificial Sequence

275 <220> FEATURE:

276 <223> OTHER INFORMATION: Bidirectional promoter

278 <400> SEQUENCE: 7

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279 agatctgcag ggtcgcctcg tggtcgaggc cacacgcgtc accttaatat gcgaagtgga 60
280 ccgatctcg agtttaccac tccctatcag tgatagagaa aagtgaaagt cgagtttacc 120
281 actccctatc agtgatagag aaaagtgaag gtcgagttta ccactcccta tcagtgatag 180
282 agaaaagtga aagtcgagtt taccactccc tatcagtgat agagaaaagt gaaagtcgag 240
283 tttaccactc cctatcagt atagagaaaa gtgaaagtcg agtttaccac tccctatcag 300
284 tgatagagaa aagtgaagtc cgagtttacc actccctatc agtgatagag aaaagtgaag 360
285 gtcgagctcg gtacccgggt cgagtaggcg tgtacggtgg gaggcctata taagcagagc 420
286 tcgtttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 480
287 aagacaccgg gaccgatcca gcctccgcgg cccgaattc 520

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289 <210> SEQ ID NO: 8

290 <211> LENGTH: 450

291 <212> TYPE: DNA

292 <213> ORGANISM: Artificial Sequence

294 <220> FEATURE:

295 <221> NAME/KEY: mRNA

296 <222> LOCATION: (382)...(450)

298 <220> FEATURE:

299 <223> OTHER INFORMATION: Tetracycline-responsive PhCMV-1 promoter

301 <400> SEQUENCE: 8

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302 gaattcctcg agtttaccac tccctatcag tgatagagaa aagtgaagtc cgagtttacc 60
303 actccctatc agtgatagag aaaagtgaag gtcgagttta ccactcccta tcagtgatag 120
304 agaaaagtga aagtcgagtt taccactccc tatcagtgat agagaaaagt gaaagtcgag 180
305 tttaccactc cctatcagt atagagaaaa gtgaaagtcg agtttaccac tccctatcag 240
306 tgatagagaa aagtgaagtc cgagtttacc actccctatc agtgatagag aaaagtgaag 300
307 gtcgagctcg gtacccgggt cgagtaggcg tgtacggtgg gaggcctata taagcagagc 360
308 tcgtttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 420
309 aagacaccgg gaccgatcca gcctccgcgg 450

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311 <210> SEQ ID NO: 9

312 <211> LENGTH: 450

313 <212> TYPE: DNA

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/874,389B

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TIME: 14:14:59

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\09252003\I874389B.raw

L:692 M:258 W: Mandatory Feature Missing, <220> Tag not found for SEQ ID#:22